

Digital, multiplexed measurements of up to 550 mRNAs in clinically relevant sample types using the nCounter Analysis System

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The nCounter Gene Expression System utilizes color-coded molecular barcodes to digitally count nucleic acid molecules in solution. The system is capable of measuring over 550 different nucleic acid species in a single reaction without reverse transcription or PCR amplification. The lack of enzymes allows for direct measurements of mRNA from a variety of input materials including degraded RNA (e.g. from formalin-fixed paraffin-embedded (FFPE) tissues) or crude cell lysates (e.g. from tissue or blood). The system can also be used to detect dsDNA fragments, allowing for a large range of potential experimental applications. Due to its ease of use, high multiplexing capabilities, and digital readout the system is ideal for validation studies of gene sets derived from discovery platforms such as next generation sequencing or microarrays. New applications of the nCounter System such as miRNA profiling and DNA copy number measurement are currently under development.

Nanostring nCounter System Publications

*Geiss et al, "Direct multiplexed measurement of gene expression with color-coded probe pairs" *Nature Biotechnology* 26(3):317 (2008)

*Amit, I et. al. Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. [*Science*](#) 329: 257-263 (2009)

*Palamanda JR, et. al. Evaluation of CYP1A1 and CYP2B1/2 m-RNA Induction in Rat Liver Slices Using the NanoString® Technology: A Novel Tool for Drug Discovery Lead Optimization. [*Drug Metabolism Letters*](#) 2009 Aug;3(3):171-5. Epub 2009 Aug 1.

*Payton JE, et. al. High throughput digital quantification of mRNA abundance in primary human acute myeloid leukemia samples. [*The Journal of Clinical Investigation*](#) 119(6): 1714-1726 (2009).

*Vladislav MA, et al. Multiplexed measurements of gene signatures in different analytes using the NanoString nCounter Assay System [*BMC Research Notes*](#) 2: 80 (2009).

*Yi-Hsien Su, et.al. A Perturbation Model of the Gene Regulatory Network for Oral and Aboral Ectoderm Specification in the Sea Urchin Embryo. [*Developmental Biology*](#) 329: 410-421 (2009).

*Birtwell, S, et. al. Microparticle encoding technologies for high-throughput multiplexed suspension assays. [*Integrative Biology*](#) 1: 227-436 (2009).